

(1) GENERAL INFORMATION

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTEASE-6

(iii) NUMBER OF SEQUENCES: 9

(iv) ~~CORRESPONDENCE ADDRESS:~~

(A) ADDRESSEE: SmithKline Beecham Corporation

(B) STREET: 709 Swedeland Road

(C) CITY: King of Prussia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: UNKNOWN

(B) FILING DATE: HEREWITH

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/018,961

(B) FILING DATE: 05 JUNE 1996

(A) APPLICATION NUMBER: 60/020,344

(B) FILING DATE: 23 MAY 1996

(A) APPLICATION NUMBER: 60/017,949

(B) FILING DATE: 20 May 1996

(viii) ATTORNEY/AGENT INFORMATION:

(ix) TELECOMMUNICATION INFORMATION:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

- 65 -

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 285
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365
 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT GGTGGAAGAG	60
CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGCG AGCTGTTTCTAG GCCCCATATG	120
ATCGAGGACA TCCAGCGGGC AGGCTCTGGA TCTCGGCGGG ATCAGGCCAG GCAGCTGATC	180
ATAGATCTGG AGACTCGAGG GAGTCAGGCT CTTCTTTTGT TCATCTCCTG CTTAGAGGAC	240
ACAGGCCAGG ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCTG	300
AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGATTCTG CAAACCAGAG	360
GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT CTGGAGGATT CGGTGATGTC	420
GGTGCTCTTG AGAGTTTGAG GGGAAATGCA GATTTGGCTT ACATCCTGAG CATGGAGCCC	480
TGTGGCCACT GCCTCATTAT CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC	540
CGCACTGGCT CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTT	600
ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT GCTGGAGCTG	660
GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCCTGGTGG TCATTCTCTC TCACGGCTGT	720
CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT GTCTACGGCA CAGATGGATG CCCTGTGTCTG	780
GTCGAGAAGA TTGTGAACAT CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC	840
AAGCTCTTTT TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC	900
TCCACTTCCC CTGAAGACGA GTCCCCCTGGC AGTAACCCCG AGCCAGATGC CACCCCGTTC	960
CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT CTAGTTTGCC CACACCCAGT	1020
GACATCTTTG TGTCCTACTC TACTTTCCCA GGTTTTGTCTT CCTGGAGGGA CCCCAGAGT	1080
GGCTCCTGGT ACGTTGAGAC CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC	1140
CTGCAGTCCC TCCTGCTTAG GGTGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG	1200
ATGCCTGGTT GCTTTAATTT CCTCCGGAAG AAACCTTTCT TTAAACATC ATAAGGCCAG	1260
GGCCCCCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC TGCCCCAGGC CTGAAAGAGG	1320
CTGAGGCCCTG GACTTTCCTG CAACTCAAGG ACTTTGNAGC CGGCACAGG TCTGCTCTTT	1380
CTCTGCCAGT GACAGACAGG CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT	1440
GGAGGAAGAG GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT	1500
CCAGGGCTAG TGAATTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG CAGGGATTAA	1560
CCTCTGCACT ACTGACAT	1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAAATGGT	GCTGGCTTTG	CTGGAGCTGG	CGCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT	GCGTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG	TCTACGGCAC	AGATGGATGC	CCTGTGTCGG	TCGAAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGCCC	CAGCCTGGGA	GGGAAGCCCA	AGCTCTTTTT	CATCCAGGCC	240
TGTGGTGGGG	AGCAGAAAGA	CCATGGGTTT	GAGGTGGCCT	CCACTTCCCC	TGAAGACGAG	300
TCCCCTGGCA	GTAACCCCGA	GCCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAGCTGG	ACGCCATATC	TAGTTTGCCC	ACACCCAGTG	ACATCTTTGT	GTCCTACTCT	420
ACTTTCCTCAG	GTTTTGTTTC	CTGGAGGGAC	CCCAAGAGTG	GCTCCTGGTA	CGTTGAGACC	480
CTGGACGACA	TCTTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTCGCTAATG	CTGTTTCGGT	GAAAGGGATT	TATAAACAGA	TGCCTGGTTG	CTTTAATTTT	600
CTCCGGAAAA	AACTTTTCTT	TTAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Leu	Ala	Leu	Leu	Glu	Leu	Ala	Arg	Gln	Asp	His	Gly	Ala	Leu
1				5					10					15	
Asp	Cys	Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	Ala	Ser	His
			20					25						30	
Leu	Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys	Pro	Val	Ser
			35				40					45			
Val	Glu	Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys	Pro	Ser	Leu
			50			55						60			
Gly	Gly	Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Ala	Cys	Gly	Gly	Glu	Gln

65		70		75		80									
Lys	Asp	His	Gly	Phe	Glu	Val	Ala	Ser	Thr	Ser	Pro	Glu	Asp	Glu	Ser
			85						90					95	
Pro	Gly	Ser	Asn	Pro	Glu	Pro	Asp	Ala	Thr	Pro	Phe	Gln	Glu	Gly	Leu
			100					105					110		
Arg	Thr	Phe	Asp	Gln	Leu	Asp	Ala	Ile	Ser	Ser	Leu	Pro	Thr	Pro	Ser
			115					120					125		
Asp	Ile	Phe	Val	Ser	Tyr	Ser	Thr	Phe	Pro	Gly	Phe	Val	Ser	Trp	Arg
			130					135					140		
Asp	Pro	Lys	Ser	Gly	Ser	Trp	Tyr	Val	Glu	Thr	Leu	Asp	Asp	Ile	Phe
			145					150					155		160
Glu	Gln	Trp	Ala	His	Ser	Glu	Asp	Leu	Gln	Ser	Leu	Leu	Leu	Arg	Val
			165						170					175	
Ala	Asn	Ala	Val	Ser	Val	Lys	Gly	Ile	Tyr	Lys	Gln	Met	Pro	Gly	Cys
			180						185					190	
Phe	Asn	Phe	Leu	Arg	Lys	Lys	Leu	Phe	Phe	Met					
			195						200						

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CCGCCATGGA CGAAGCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT
CCGGAG

60

66

00961203 092401
174250 102200

[illegible]

(i) APPLICANT: DIXIT, VISHVA M.
HE, WEI-WU
KIKLY, KRISTINE K.
RUBEN, STEVEN M.

(iii) NUMBER OF SEQUENCES: 11

v) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Ratner & Prestia
(B) STREET: P.O. Box 980
(C) CITY: Valley Forge
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19482

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

1) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/952,936
- (B) FILING DATE: 08-MAY-1997
- (C) CLASSIFICATION: UNKNOWN

11) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/013,361
(B) FILING DATE: 05-JUN-1996

(A) APPLICATION NUMBER: 60/020,344
(B) FILING DATE: 23-MAY-1996

(A) APPLICATION NUMBER: 60/017,949
(B) FILING DATE: 20-MAY-1996

(A) NAME: Prestia, Paul F
(B) REGISTRATION NUMBER: 23,031
(C) REFERENCE/DOCKET NUMBER: p50483-2

(A) TELEPHONE: 610-407-0700
(B) TELEFAX: 610-407-0700
(C) TELEX: 346159

(2) INFORMATION FOR SEQ ID NO:1:

[illegible]

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Glu	Ala	Asp	Arg	Arg	Leu	Leu	Arg	Arg	Cys	Arg	Leu	Arg	Leu	
1				5					10						15	
Val	Glu	Glu	Leu	Gln	Val	Asp	Gln	Leu	Trp	Asp	Val	Leu	Leu	Ser	Arg	
			20					25						30		
Glu	Leu	Phe	Arg	Pro	His	Met	Ile	Glu	Asp	Ile	Gln	Arg	Ala	Gly	Ser	
		35					40					45				
Gly	Ser	Arg	Arg	Asp	Gln	Ala	Arg	Gln	Leu	Ile	Ile	Asp	Leu	Glu	Thr	
	50					55					60					
Arg	Gly	Ser	Gln	Ala	Leu	Pro	Leu	Phe	Ile	Ser	Cys	Leu	Glu	Asp	Thr	
	65				70					75					80	
Gly	Gln	Asp	Met	Leu	Ala	Ser	Phe	Leu	Arg	Thr	Asn	Arg	Gln	Ala	Gly	
				85					90					95		
Lys	Leu	Ser	Lys	Pro	Thr	Leu	Glu	Asn	Leu	Thr	Pro	Val	Val	Leu	Arg	
		100						105						110		
Pro	Glu	Ile	Arg	Lys	Pro	Glu	Val	Leu	Arg	Pro	Glu	Thr	Pro	Arg	Pro	
	115						120					125				
Val	Asp	Ile	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Val	Gly	Ala	Leu	Glu	Ser	
	130					135					140					
Leu	Arg	Gly	Asn	Ala	Asp	Leu	Ala	Tyr	Ile	Leu	Ser	Met	Glu	Pro	Cys	
	145				150					155				160		
Gly	His	Cys	Leu	Ile	Asn	Asn	Val	Asn	Phe	Cys	Arg	Glu	Ser	Gly		
				165				170						175		
Leu	Arg	Thr	Arg	Thr	Gly	Ser	Asn	Ile	Asp	Cys	Glu	Lys	Leu	Arg	Arg	
			180					185					190			
Arg	Phe	Ser	Ser	Leu	His	Phe	Met	Val	Gln	Val	Lys	Gly	Asp	Leu	Thr	
	195						200					205				
Ala	Lys	Lys	Met	Val	Leu	Ala	Leu	Leu	Glu	Leu	Ala	Arg	Gln	Asp	His	
	210					215					220					
Gly	Ala	Leu	Asp	Cys	Cys	Val	Val	Val	Ile	Leu	Ser	His	Gly	Cys	Gln	
	225				230					235				240		
Ala	Ser	His	Leu	Gln	Phe	Pro	Gly	Ala	Val	Tyr	Gly	Thr	Asp	Gly	Cys	
			245					250						255		
Pro	Val	Ser	Val	Glu	Lys	Ile	Val	Asn	Ile	Phe	Asn	Gly	Thr	Ser	Cys	
		260						265					270			
Pro	Ser	Leu	Gly	Gly	Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Ala	Cys	Gly	
	275						280					285				
Gly	Glu	Gln	Lys	Asp	His	Gly	Phe	Glu	Val	Ala	Ser	Thr	Ser	Pro	Glu	
	290					295					300					
Asp	Glu	Ser	Pro	Gly	Ser	Asn	Pro	Glu	Pro	Asp	Ala	Thr	Pro	Phe	Gln	
	305					310				315				320		
Glu	Gly	Leu	Arg	Thr	Phe	Asp	Gln	Leu	Asp	Ala	Ile	Ser				

Asp Ile Phe Glu Gln Ala His Ser Glu Asp Leu Gln Ser Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG	AAGCGGATCG	GCGGCTCCTG	CGGCGGTGCC	GGCTGCGGCT	GGTGAAGAG	60
CTGCAGGTGG	ACCAGCTCTG	GGACGTCCTG	CTGAGCCGCG	AGCTGTTTCAG	GCCCCATATG	120
ATCGAGGACA	TCCAGCGGGC	AGGCTCTGGA	TCTCGGCGGG	ATCAGGCCAG	GCAGCTGATC	180
ATAGATCTGG	AGACTCGAGG	GAGTCAGGCT	CTTCCTTTGT	TCATCTCCTG	CTTAGAGGAC	240
ACAGGCCAGG	ACATGCTGGC	TTGTTTTCTG	CGAACTAACA	GGCAAGCAGG	AAAGTTGTCTG	300
AAGCCAACCC	TAGAAAACCT	TACCCGAGTG	GTGCTCAGAC	CAGAGATTCG	CAAACCAGAG	360
GTTCTCAGAC	CGGAAACACC	CAGACCATGG	GACATTGGTT	CTGGAGGATT	CGGTGATGTC	420
GGTGCTCTTG	AGAGTTTGAG	GGGAAATGCA	GATTTGGCTT	ACATCCTGAG	CATGGAGCCC	480
TGTGGCCACT	GCCTCATTAT	CAACRATGTG	AACTTCTGCC	GTGAGTCCCG	GCTCCGCACC	540
CGCACTGGCT	CCAACATCGA	CTGTGAGAAG	TTGCGGCGTC	GCTTCTCCTC	GCTGCATTTT	600
ATGGTGGAGG	TGAAGGGCGA	CCTGACTGCC	AAGAAAATGG	TGCTGGCTTT	GCTGGAGCTG	660
GCGCGGCAGG	ACCACGGTGC	TCTGGACTGC	TGCGTGGTGG	TCATTCTCTC	TCACGGCTGT	720
CAGGCCAGCC	ACCTGCAGTT	CCCAGGGGCT	GTCTACGGCA	CAGATGGATG	CCCTGTGTCTG	780
GTGAGAGAAG	TTGTGAACAT	CTTCAATGGG	ACCAGCTGCC	CCAGCCTGGG	AGGGAAGCCC	840
AAGCTCTTTT	TCATCCAGGC	CTGTGGTGGG	GAGCAGAAAG	ACCATGGGTT	TGAGGTGGCC	900
TCCACTTCCC	CTGAAGACGA	GTCCCTTGGC	AGTACCCCG	AGCCAGATGC	CACCCCCTTC	960
CAGGAAGGTT	TGAGGACCTT	CGACCACTG	GACGCCATAT	CTAGTTTGCC	CACACCCAGT	1020
GACATCTTTT	TGTCCTACTC	TACTTTCCCA	GGTTTTGTTT	CCTGGAGGGA	CCCCAAGAGT	1080
GGCTCCTGGT	ACGTTGAGAC	CCTGGACGAC	ATCTTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
ATGCCTGGTT	GCTTTAATTT	CCTCCGGAAA	AAACTTTTCT	TTAAAACATC	ATAAGGCCAG	1200
GGCCCCTCAC	CCTGCCTTAT	CTTGCACCCC	AAAGCTTTCC	TGCCCCAGGC	CTGAAAGAGG	1260
CTGAGGCCCTG	GACTTTCCTG	CAACTCAAGG	ACTTTGNAGC	CGGCACAGGG	TCTGCTCTTT	1320
CTCTGCCAGT	GACAGACAGG	CTCTTAGCAG	CTTCCAGATT	GACGACAAGT	GCTGAACAGT	1380
GGAGGAAGAG	GGACAGATGA	ATGCCGTGGA	TTGCACGTGG	NCTCTTGAGC	AGTGGCTGGT	1440
CCAGGGCTAG	TGACTTGGTG	TCCCATGATC	CCTGTGTTGG	TCTCTAGGAG	CAGGGATTAA	1500
CCTCTGCACT	ACTGACAT					1560
						1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAAATGGT	GCTGGCTTTG	CTGGAGCTGG	CGCGGCAGGA	CCACGGTGCT	60
CTGGACTGCT	GCGTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CCTGCAGTTC	120
CCAGGGGCTG	TCTACGGCAC	AGATGGATGC	CCTGTGTCGG	TCGAAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGCCC	CAGCCTGGGA	GGGAAGCCCC	AGCTCTTTTT	CATCCAGGCC	240
TGTGGTGGGG	AGCAGAAAGA	CCATGGGTTT	GAGGTGGCCT	CCACTTCCCC	TGAAGACGAG	300
TCCCCTGGCA	GTAACCCCGA	GCCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAGCTGG	ACGCCATATC	TAGTTTGCCC	ACACCCAGTG	ACATCTTTGT	GTCCTACTCT	420
ACTTTCCAG	GTTTTGTTTC	CTGGAGGGAC	CCCAAGAGTG	GCTCCTGGTA	CGTTGAGACC	480
CTGGACGACA	TCTTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTCGCTAATG	CTGTTTCGGT	GAAAGGGATT	TATAAACAGA	TGCCTGGTTG	CTTTAATTTT	600
CTCCGGAAAA	AACTTTTTCT	TTAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
1 5 10 15
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
20 25 30
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
35 40 45
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
50 55 60
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln
65 70 75 80
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser
85 90 95
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu
100 105 110
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser
115 120 125
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg
130 135 140
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe
145 150 155 160
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val
165 170 175
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys
180 185 190
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met
195 200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

34

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE SEQUENCE
 TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG

60

(1) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: CONA

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAGC

29

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCAT CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTTT
CCGGAG

60
66

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Gly Gly
1 5

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